



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 222738

TO: Minh-Tam Davis
Location: REM/3A24/3C18
Art Unit: 1642
Wednesday, April 25, 2007

Case Serial Number: 10/728019

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A55
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

The Oct 1996 version of this sequence has 672 aa; the record and alignment are attached.

These results will not appear on SCORE.

Please feel free to contact me if you have any questions or would like to rework the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold





All Databases

Enter Text Here

Reset

UniProt Home
UniProtKB/Swiss-Prot
UniProtKB/TrEMBL
UniSave
UniSave/Batch

EBI UniProt UniSave

The UniProtKB Sequence/Annotation Version Archive (UniSave) is a repository of UniProtKB/Swiss-Prot and UniProtKB/TrEMBL entry versions.

Primary accession number or entry name: **P53349**

Go!

Date: day-month-year (e.g. 30-11-1998 or 30-NOV-1998) or year-month

Save

UniProtKB

P53349

Later >>

Release: 34.0 Date: 01-OCT-1996

ID MEKK_MOUSE STANDARD; PRT; 672 AA.
AC P53349
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MEK KINASE (EC 2.7.1.-) (MEKK).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE; 93227040.
RA LANGE-CARTER C.A., PLEIMAN C.M., GARDNER A.M., BLUMER K.J.,
RA JOHNSON G.L.;
RL SCIENCE 260:315-319(1993).
CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAP KINASE KINASE 1
CC (MEK1) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART AND SPLEEN
CC A LOWER LEVEL EXPRESSION IS SEEN IN THE LIVER.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. BELONGS TO THE MAP KINASE KINASE KINASE FAM.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; L13103; G293730; -.
KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW PHOSPHORYLATION.
FT DOMAIN 403 672 PROTEIN KINASE (BY SIMILARITY).
FT NP_BIND 409 416 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT_SITE 529 529 BY SIMILARITY.
SQ SEQUENCE 672 AA; 72983 MW; 67CE46FE CRC32;
MVTAVPAVFS KLVTMLNASG STHFTRMRRR LMAIADEVEI AEVIQLGVED TVDGHQDSLQ
AVAPTSCLEN SSLEHTVHRE KTGKGLSATR LSASSEDISD RLAGVSVGLP SSTTTEQPKI
AVQTKGRPHS QCLNSSPLSH AQLMFPAISA PCSSAPSVPD ISKHRPQAFV PCKIPASAPQ
TQRKFSLQFQ RNCSEHRDSD QLSPVFTQSR PPPSSNIHRP KPSRPVPGST SKLGDATKS;
MTLDLGSASR CDSFSGGGN SGNVIPSDE TVFTPVEDKC RLDVNTLNS SIEDLLEASI
PSSDTTVTFK SEVAVLSPEK AENDDTYKDD VNHNQCKEK MEAEVEEALA IAMAMSASQI
ALPIVPQLQV ENGEDIIIIQ QDTPETLPGH TKAKQPYRED AEWLKGOQIG LGAFSSCYQI
QDVGTTILMA VKQVTYVRNT SSEQEEVVEA LREEIRMMGH LNHPNIIRML GATCEKSNIYI
LFIEWMAGGS VAHLLSKYGA FKESVVINYT EQLLRGLSYL HENQIIHRDV KGANLLIDS;
QQLRIADFG AAARLASKGT GAGEFQGOQLL GTIAFMAPEV LRGOQYGRSC DVWSVGCAL;
PVCCHVRRRI RRGVGHVHVA LKFAVGRFTH DDTGSHVGRG LKRVNVCLE LKQGRRRRRI

EMACAKPPWN AERHSNHLAL IFKIASATTA PSTPSHLSFG LRDVAVRLE LQPQDRPPI
ELLKHPVFRT TW

//

[Show Help](#)

[Terms of Use](#) | [EBI Funding](#) | [Contact EBI](#) | © European Bioinformatics Institute 2006-2007. EBI is an Outstation of the [European Molecular Biology Laboratory](#)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2007, 10:13:58 ; Search time 1 Seconds
(without alignments)
1.003 Million cell updates/sec

Title: US-10-728-019-3
Perfect score: 7732
Sequence: 1 MAAAGDRASSGFFGAAAA.....PQDRPPSRELLKHPVFRITW 1493

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 672 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : new.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3467	44.8	672	1	MEKKMOUSE01OCT1996 Entered [darnold]

ALIGNMENTS

RESULT 1
MEKKMOUSE01OCT1996
; Entered [darnold 25-Apr-07 10:06]
MEKKMOUSE01OCT1996

Query Match 44.8%; Score 3467; DB 1; Length 672;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 822 MVTAVPAVFSKLVMTLNASGTHETRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDSLQ 881
Db 1 MVTAVPAVFSKLVMTLNASGTHETRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDSLQ 60

Qy 882 AVAPTSCLENSLEHTVHREKTGKLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKP 941
Db 61 AVAPTSCLENSLEHTVHREKTGKLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKP 120

Qy 942 AVQTKGRPHSQCLNSSPLSHAQLMFPAPAPCSGAPSVDPDISKHQPQAFVCKIPSPQ 1001
Db 121 AVQTKGRPHSQCLNSSPLSHAQLMFPAPAPCSGAPSVDPDISKHQPQAFVCKIPSPQ 180

Qy 1002 TORKEFQFORNCSEHRDSDQLSPVFTQSRPPPSNIIHRPKPSRPVPGSTSKLGDATKSS 1061
Db 181 TORKEFQFORNCSEHRDSDQLSPVFTQSRPPPSNIIHRPKPSRPVPGSTSKLGDATKSS 240

Qy 1062 MTLDLGSASRCDDSPGGGNSGNAVIPSDETVFTPVDEKCRLDVNTLNSSIEDLLEASM 1121